

Resource Summary Report

Generated by [SPARC SAWG](#) on Sep 19, 2026

ADMIXTURE

RRID:SCR_001263

Type: Tool

Proper Citation

ADMIXTURE (RRID:SCR_001263)

Resource Information

URL: <https://dalexander.github.io/admixture/download.html>

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Description: A software tool for maximum likelihood estimation of individual ancestries from multilocus SNP genotype datasets. It uses the same statistical model as STRUCTURE but calculates estimates much more rapidly using a fast numerical optimization algorithm. It uses a block relaxation approach to alternately update allele frequency and ancestry fraction parameters. Each block update is handled by solving a large number of independent convex optimization problems, which are tackled using a fast sequential quadratic programming algorithm. Convergence of the algorithm is accelerated using a novel quasi-Newton acceleration method., THIS RESOURCE IS NO LONGER IN SERVICE. Documented on September 16,2025.

Abbreviations: ADMIXTURE

Synonyms: ADMIXTURE: fast ancestry estimation

Resource Type: software resource

Defining Citation: [PMID:19648217](#)

Keywords: ancestry, macos x, linux, admixture, allele, genome, single nucleotide polymorphism, bio.tools

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: ADMIXTURE

Resource ID: SCR_001263

Alternate IDs: biotools:admixture, OMICS_02077

Alternate URLs: <http://www.genetics.ucla.edu/software/admixture/>

Record Creation Time: 20220129T080206+0000

Record Last Update: 20260912T195522+0000

Ratings and Alerts

No rating or validation information has been found for ADMIXTURE.

No alerts have been found for ADMIXTURE.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 2699 mentions in open access literature.

Listed below are recent publications. The full list is available at [SPARC SAWG](#) .

McFarland LN, et al. (2026) The dilution effect of stocking and the loss of wildness among North American mallards. *Current biology* : CB.

Sharma M, et al. (2026) Improved reference assembly and core collection resequencing to facilitate exploration of important agronomical traits for the improvement of oilseed crop, *Carthamus tinctorius* L. *GigaScience*, 15.

Kore P, et al. (2026) Interplay between Genetic Ancestry, Self-reported Race and Ethnicity, and Clinical Factors in Pediatric Acute Lymphoblastic Leukemia: A REDIAL Consortium Report. *Cancer epidemiology, biomarkers & prevention : a publication of the American Association for Cancer Research*, cosponsored by the American Society of Preventive Oncology, 35(5), 710.

Chung C, et al. (2026) Ancestrally Diverse Autologous Patient-Derived Organoid-Immune Cell Coculture Platform for Addressing Immunotherapeutic Outcome Disparities in High-Grade Endometrial Cancer. *Cancer research communications*, 6(3), 657.

Liu Q, et al. (2026) Structural variation drives praziquantel response and host adaptation in *Schistosoma japonicum*. *iScience*, 29(6), 116118.

Denis H, et al. (2026) Contrasting population structures of reef-building corals and their algal symbionts inform adaptive potential across the western Pacific. *Current biology* : CB, 36(11), 2808.

Mohanty JK, et al. (2026) Trans-QTL Alliance of HKT1 and PHL7 Modulate Salinity Stress Tolerance and Enhance Crop Yield Endurance. *Plant biotechnology journal*, 24(3), 1166.

Frimer M, et al. (2026) Comprehensive Molecular Characterization of High-Grade Endometrial Cancer in an Ancestrally Diverse Cohort. *bioRxiv* : the preprint server for biology.

Khan KD, et al. (2026) Genomic insights into the admixture and diversity of Kerala crossbred cattle. *Scientific reports*, 16(1).

Er??en M, et al. (2026) Population Structure of Genotypes and Genome-Wide Association Studies of Cannabinoids and Terpenes Synthesis in Hemp (*Cannabis sativa* L.). *Plants* (Basel, Switzerland), 15(2).

Alves da Quinta D, et al. (2025) Genetic Ancestry, Intrinsic Tumor Subtypes, and Breast Cancer Survival in Latin American Women. *Cancer research communications*, 5(7), 1070.

Chen H, et al. (2025) Chromosome-level genome assembly of *Pinus massoniana* provides insights into conifer adaptive evolution. *GigaScience*, 14.

Saoud C, et al. (2025) Germline pathogenic variants in DNA repair pathways: a key feature in a significant subset of translocation-associated sarcomas. *NPJ precision oncology*, 9(1), 133.

Hu K, et al. (2025) Development and Application of MiMouse, a Comprehensive Genomic Profiling Panel for Credentialing Mouse Tumor Models. *Cancer research communications*, 5(10), 1910.

Garsmeur O, et al. (2025) The genomic footprints of wild *Saccharum* species trace domestication, diversification, and modern breeding of sugarcane. *Cell*, 188(25), 7252.

Xiong J, et al. (2025) The genomic history of East Asian Middle Neolithic millet- and rice-agricultural populations. *Cell genomics*, 100976.

Chen H, et al. (2025) Fifteenth century CE Bolivian maize reveals genetic affinities with ancient Peruvian maize. *eLife*, 14.

Siu JHY, et al. (2025) Early lymph node T follicular helper cell signalling hub drives influenza vaccine response in an ancestrally diverse cohort. *EBioMedicine*, 122, 106036.

Arshad F, et al. (2025) A comprehensive water buffalo pangenome reveals extensive structural variation linked to population-specific signatures of selection. *GigaScience*, 14.

Ran J, et al. (2025) Ancient genomes reveal basal Asian ancestries and dynamic population interactions over time on the southern Tibetan Plateau. *iScience*, 28(11), 113676.